Claims

1. A method for analyzing a nucleic acid sample, the method comprising:

   (a) tagging sequence specific sites of the nucleic acid sample;

   (b) scanning the nucleic acid sample; and

   (c) analyzing the scan of the nucleic acid sample.

2. The method of claim 1 wherein said tagging step further comprises tagging with a sequence specific tag.

3. The method of claim 1 wherein said scanning step comprises utilizing a scanning probe microscope.

4. The method of claim 1 wherein said scanning step comprises utilizing an atomic force microscope.

5. The method of claim 1 wherein said scanning step the comprises utilizing a near field optical microscope.

6. The method of claim 1 wherein said analyzing step comprises analyzing the scan using a computer.

7. The method of claim 1 wherein said sequence-specific tag is chosen from one or more of the group comprising of a restriction endonuclease, a transcription factor, a modified nucleotide, a peptide, a nucleotide, and a small molecule conjugated to a microparticle or a nanoparticle.

8. The method of claim 1 wherein the sequence-specific tag is a duplex, a triplex, or a quadruplex performing legate.

9. The method of claim 1 wherein the nucleic acid sample is DNA chosen from one or more of the group comprising a cosmid, a bacterial artificial chromosome, or a yeast artificial chromosome.

10. The method of claim 1 wherein said analyzing step further comprises creating a bar code and comparing the bar codes from different samples.

11. The method of claim 1 further comprising linearizing the nucleic acid sample.

12. The method of claim 1 further comprising cutting the nucleic acid sample with a restriction endonuclease.

13. The method of claim 12, further comprising

(a) modifying the cut nucleic acid sample with a functional group; and

(b) tethering the nucleic acid sample to a deposition surface.

14. The method of claim 13 further comprising drying the deposition surface to which the modified nucleic acid is tethered.

15. The method of claim 14 further comprising ensuring the tethered nucleic acid sample is linearly deposited on the deposition surface.

16. The method of claim 15 wherein the functional group is chosen from the group one or more of the group comprising biotin-avidin complexes, primary amines, sulfhydral groups, single stranded binding proteins, or histidine terminated oligonucleotides.

17. The method of claim 16 wherein the deposition surface is located on a dipstick.

18. The method of claim 17 wherein the deposition surface of the dipstick has specific areas for tethering different types of functional group modified nucleic sequences.

19. A method for locating the functional segments of a nucleic acid sample, the method comprising

(c) tagging sites of the nucleic acid sample;

(d) scanning the nucleic acid sample using a scanning probe microscope;

(e) analyzing the scan of the nucleic acid sample to determine the location of the functional segments of the nucleic acid sample.

20. The method of claim 19 wherein the functional segment of the nucleic acid sample is chosen from one or more of the group comprising a promoter, an enhancer, an attenuator, and a silencer.

21. The method of claim 20 further comprising linearizing the nucleic acid sample.

22. The method of claim 21 further comprising cutting the nucleic acid sample with a restriction endonuclease.

23. The method of claim 22, further comprising

(f) modifying the cut nucleic acid sample with a functional group; and

(g) tethering the modified nucleic acid sample to a deposition surface.

24. The method of claim 23 further comprising drying the deposition surface to which the modified nucleic acid sample is tethered.

25. The method of claim 24 further comprising ensuring the tethered nucleic acid sample is linearly deposited on the deposition surface.

26. The method of claim 25 wherein the functional group is chosen from one or more of the group comprising biotin-avidin complexes, primary amines, sulfhydral groups, single stranded binding proteins, or histidine terminated oligonucleotides.

27. The method of claim 26 wherein the deposition surface is located on a dipstick.

28. The method of claim 27 wherein the deposition surface of the dipstick has a specific areas for tethering different types of functional group modified nucleic acid sample.

29. A method for comparing DNA from two different sources, comprising:

(h) tagging a nucleic acid sample from a first source;

(i) tagging a nucleic acid sample from a second source;

(j) scanning the tagged nucleic acid sample from the first source;

(k) scanning the tagged nucleic acid sample from the second source;

(l) analyzing the scan from the first source and the scan from a second source using a computer; and

(m) comparing the scan from the first source to the scan from the second source.

30. The method of claim 29 wherein said scanning further comprises utilizing a scanning probe microscope.

31. The method of claim 29 wherein the comparison allows the detection of single nucleotide polymorphisms between the DNA sources.